

2010-2011

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
 FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF
 SAPAVPSGTGQTSAELEBVQRHSLVSFVVRIVPSPDFWFGVDSLDLDCGDRWREQAALDLYP
 YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSPHANSFYYPRLKALPPTIARVTLRLRQSP
 FIAPFPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTSKTRTYVRVQPA
 NNGSPCEPLEEAAECVDPNVCV

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAAGGAGCAGAGTCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACTTTGTGTTGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCAATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGTTCGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTTGTGTTTAATCCTTTTGATGACATCATTTCAAGGGAATTAAGGCTGAAAAAGA
GAAACAGAGAGGGAAGTAAAGAAATGAAACCCAAGGCACAAAAAATTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAGGACACAAGTGCGAATGTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACCGGGAACCTTTAGCAG
CAAAACAAAAAAGTAGAAAAATGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGTTGCTGTTGCCGAATACAGAAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAGAAGAGGGAACCTCCCGGAAGATCAGACCCCTGCACTGCTGAACCAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT
GAGAAATATGATAACCAAGACTTGCTGGAATGTGCCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTG
TACATGTGTTTTTCTAGCTGACCTTTTATATGTCTAAATCTGAAATAAAATAACTTTCTT
TCCACAAAAA

0967895-141504

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLTKTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGKTKNFSLLSFGEEAESEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVAAYRREKQKYALRK
QQSKKGTSREDQTLALLNQFKSLTQAIAETPENDIPETEVEDDEGWMShVLQFEDKSRKVK
DASMQDSDTFEYDPRNPFVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

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